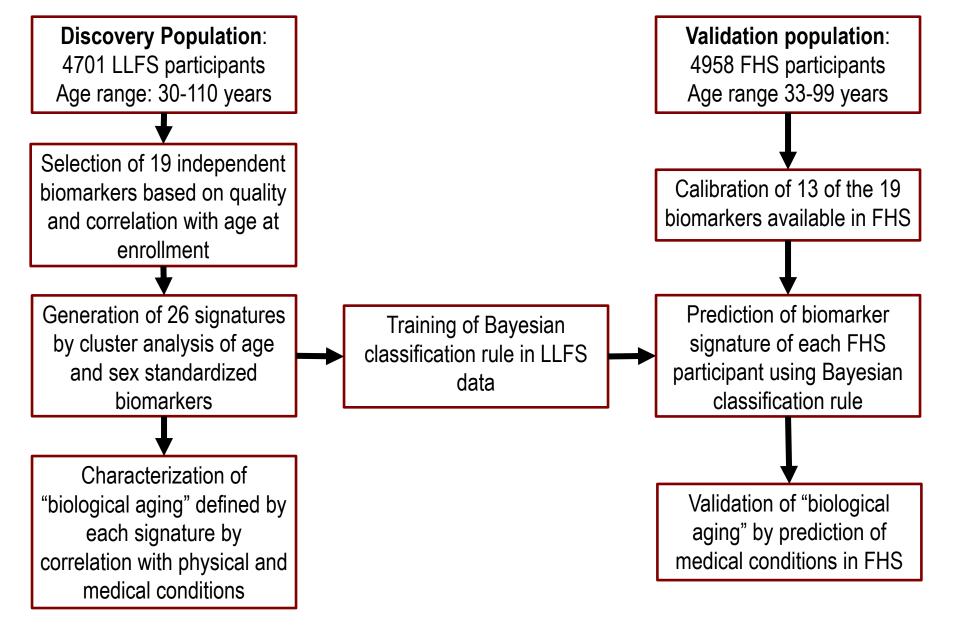
Paola Sebastiani, Bharat Thyagarajan, Fangui Sun, Nicole Schupf, Anne B Newman, Monty Montano, Thomas T Perls

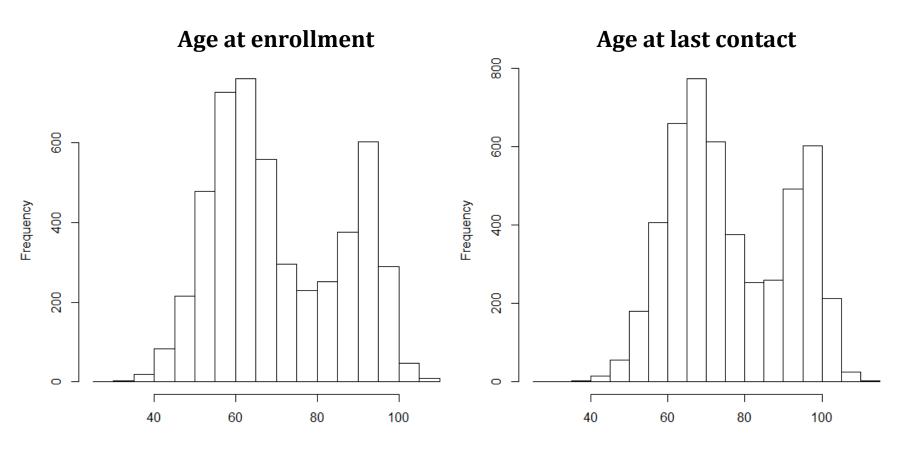
BIOMARKER SIGNATURES OF AGING: SUPPLEMENT FIGURES 1-22

Table of content

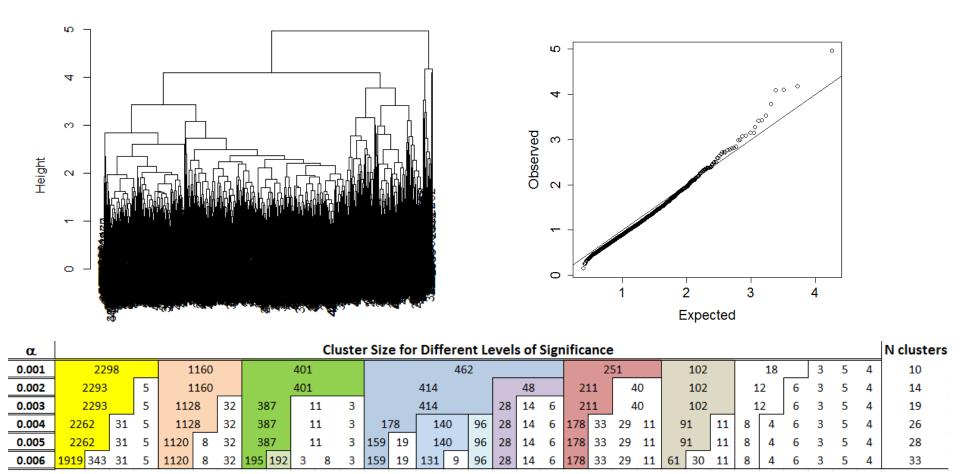
- * Supplement Figure S1: Flow chart of the analytic approach
- ★ Supplement Figure S2: Distribution of age at enrollment in LLFS
- Supplement Figure S3: Overview of cluster analysis to discover biomarker signatures
- * Supplement figure S4(a-b): age and sex distributions of biomarkers
- * Supplement Figures S5 through S17: description of 26 biomarker signatures in LLFS
- * Supplement Figure S18a through S18p: Age and sex specific distribution of 19 biomarkers in clusters 1-17. Red and blue denote females and males in cluster 1; magenta and cyan denote females and males in the cluster described in the title page
- * Supplement Figure S19: example of lab-bias in the measurement of albumin
- * Supplement Figure S20a through S20w: distribution of externally standardized biomarkers in FHS data using LLFS means and standard deviations
- Supplement Figure S21: Distribution of biomarker signatures in LLFS and FHS offspring
- Supplement Figure S22a through S22g: Reproduced biomarker signatures in FHS offspring



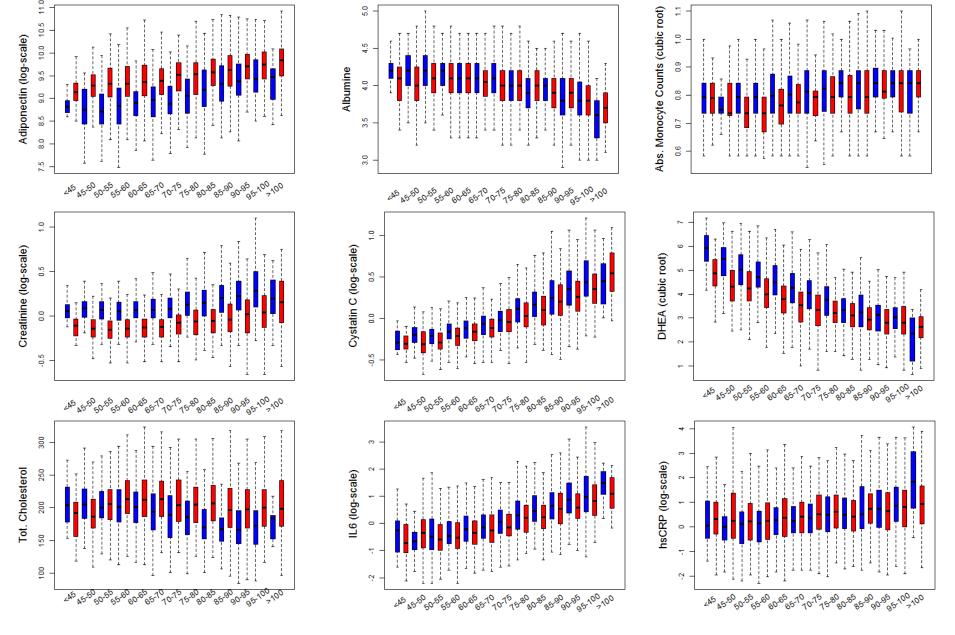
Supplement Figure S1: Flow chart of the analytic approach



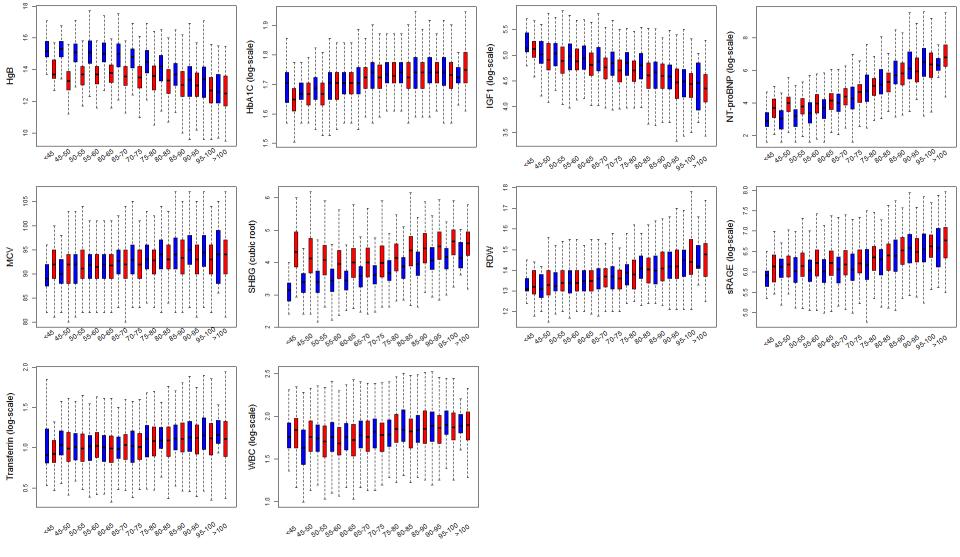
Supplement Figure S2: Distribution of age at enrollment and age at last contact in the 4701 LLFS participants included in the analysis



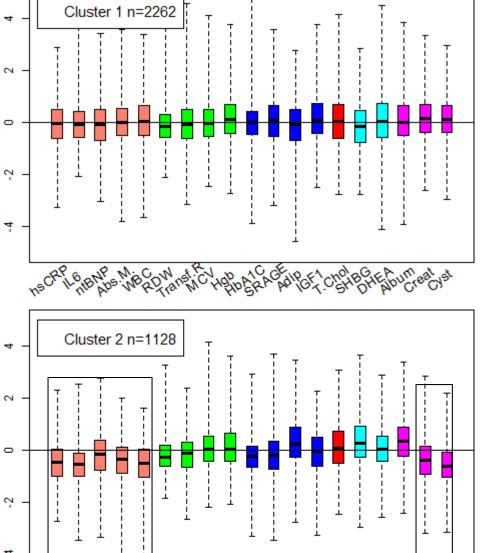
Supplement Figure S3: *Top left* – dendrogram displaying the arrangement of subject profiles by hierarchical clustering with complete linkage. The distances are normalized by the number of biomarkers (n=19). *Top right*: QQ-plot displaying the observed and expected distances used in hierarchical clustering (height of branch nodes). Departure from the diagonal line suggests that there are significant clusters in the data. *Bottom*: Cluster composition for different levels of significance a (first column). Colors track clusters that are robust with respect to different levels of significant. The number of clusters ranges from 10 for a=0.1% to 33 a=0.6% but most of the differences are in the generation of new clusters with very small number of individuals. With a= 0.4% the algorithm detects 26 clusters, and the most noticeable difference from the clusters detected with a between 0.1% and 0.3% is the split of the cluster with 462 participants into 3 smaller clusters of 96, 140 and 178 participants (Clusters highlighted in blue). For all subsequent analyses, we used the 26 clusters detected for a significance level of 0.4% that provides a good compromise between number of clusters and error rate.



Supplement Figure S4a: Age and sex distribution of selected biomarkers (blue=males, red=females.)



Supplement Figure S4b: Age and sex distribution of selected biomarkers (blue=male, red=females.). Mean and standard deviation per age group were used to define the age and sex specific z-score. Outliers were removed using 2.5% trimmed means.



Supplement Figure S5: Profiles 1 and 2

"Referent profile": biomarkers are equal to the value expected for age/sex

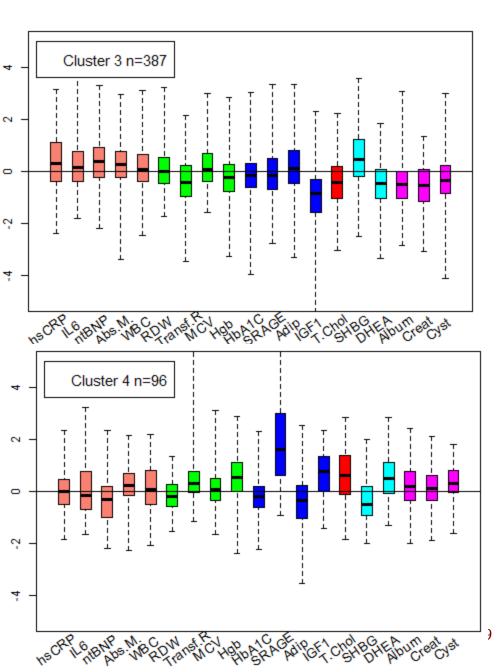
Cluster:

37% born < 1935; median age 90 63% born > 1935; median age 60 54% females

Profile 2: a group of biomarkers lower than the value expected for age/sex

Cluster:

41% born < 1935; median age 90 59% born > 1935; median age 61 55% females



Supplement Figure S6:

Profiles 3 and 4

Profile 3: higher than average inflammation, low DHEA and albumin suggesting frailty

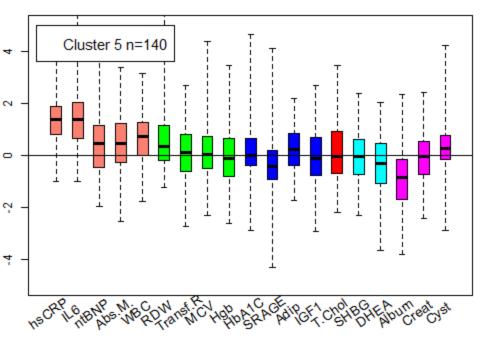
Cluster:

34% born < 1935; median age 91 66% born > 1935; median age 60 59% females

Profile 4: extremely elevated sRAGE, IGF1 and cholesterol

Cluster:

36% born < 1935; median age 92 64% born > 1935; median age 61 55% females

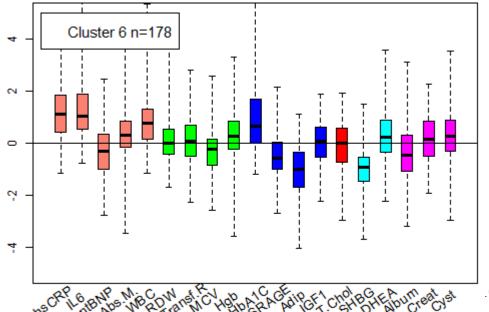


Supplement Figure S7: Profiles 5 and 6

Profile 5:

Cluster:

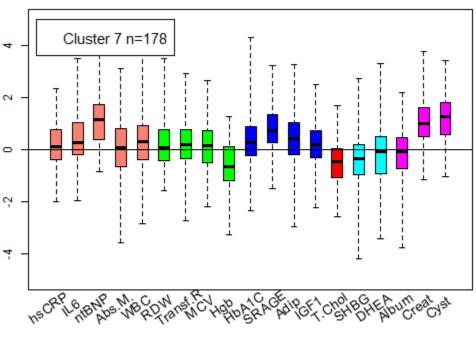
41% born < 1935; median age 91 59% born > 1935; median age 59 46% females



Profile 6:

Cluster:

36% born < 1935; median age 90 64% born > 1935; median age 62 62% females

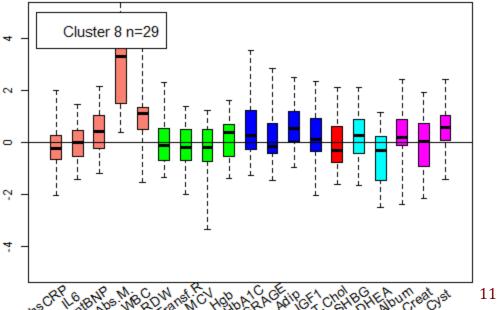


Supplement Figure S8: Profiles 7 and 8

Profile 7:

Cluster:

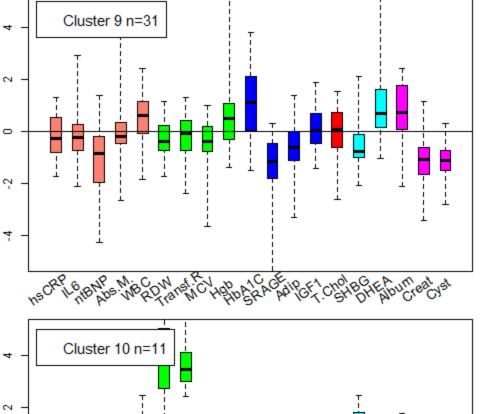
56% born < 1935; median age 92 44% born <u>></u> 1935; median age 62 55% females



Profile 8:

Cluster:

55% born < 1935; median age 91 45% born ≥ 1935; median age 58 48% females



Supplement Figure S9: Profiles 9 and 10

Profile 9:

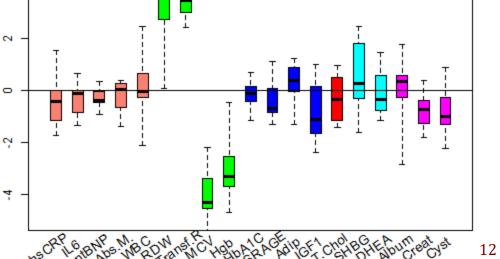
Cluster:

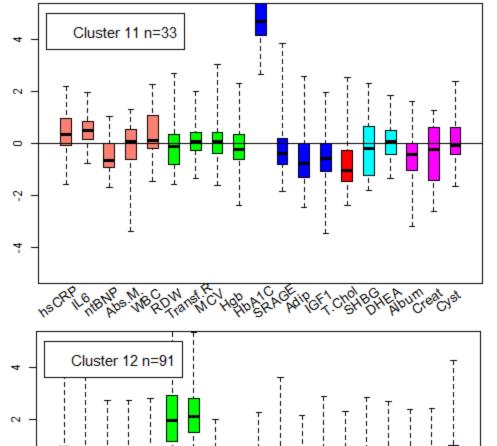
42% born < 1935; median age 87 58% born > 1935; median age 64 48% females

Profile 10:

Cluster:

45% born < 1935; median age 88 55% born > 1935; median age 52 73% females





Supplement Figure S10: Profiles 11 and 12

Profile 11:

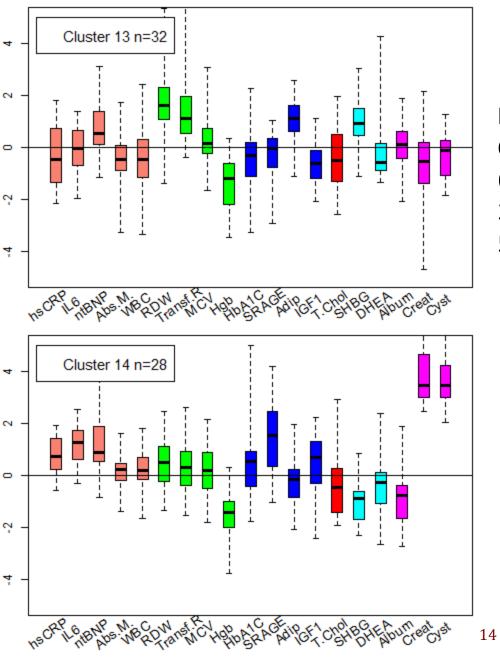
Cluster:

27% born < 1935; median age 85 73% born > 1935; median age 59 49% females

Profile 12:

Cluster:

42% born < 1935; median age 92 58% born <u>></u> 1935; median age 59 54% females



Supplement Figure S11: Profiles 13 and 14

Profile 13:

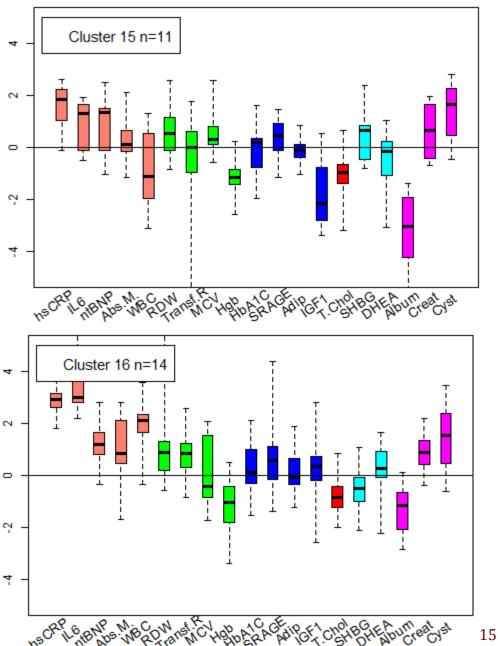
Cluster:

66% born < 1935; median age 89 34% born > 1935; median age 57 55% females

Profile 14:

Cluster:

57% born < 1935; median age 91 43% born ≥ 1935; median age 57 61% females



Supplement Figure S12: Profiles 15 and 16

Profile 15:

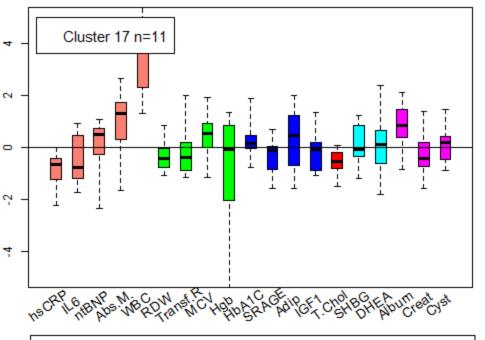
Cluster:

55% born < 1935; median age 89 45% born ≥ 1935; median age 63 73% females

Profile 16:

Cluster:

64% born < 1935; median age 92 36% born <u>></u> 1935; median age 63 29% females

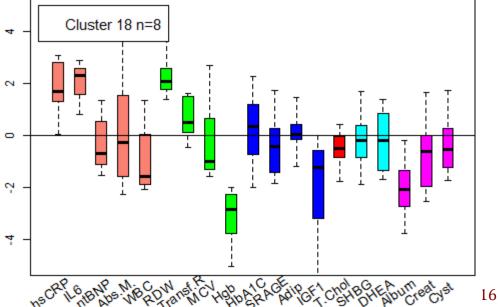


Supplement Figure S13: Profiles 17 and 18

Profile 17:

Cluster:

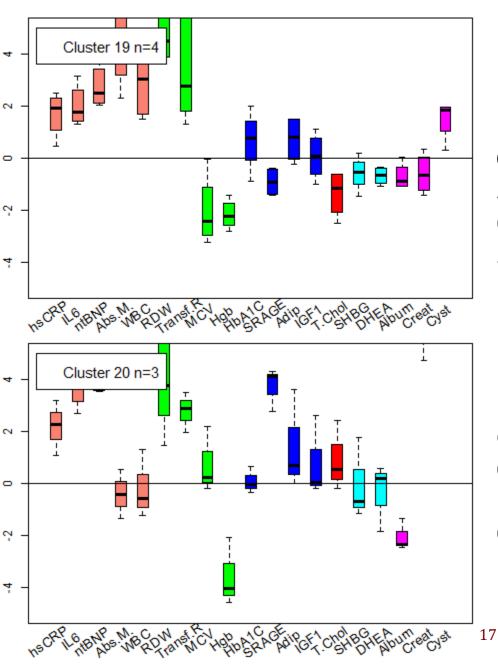
55% born < 1935; median age 90 45% born ≥ 1935; median age 61 46% females



Profile 18:

Cluster:

50% born < 1935; median age 98 40% born > 1935; median age 55 75% females



Supplement Figure S14: Profiles 19 and 20

Profile 19:

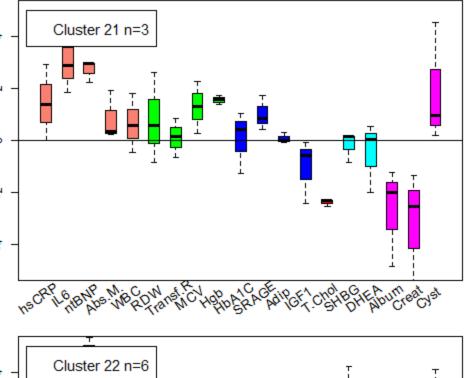
Cluster:

50% born < 1935; median age 79 60% born > 1935; median age 59 25% females

Profile 20:

Cluster:

0% born < 1935 100% born ≥ 1935; median age 57 0% females



Supplement Figure S15: Profiles 21 and 22

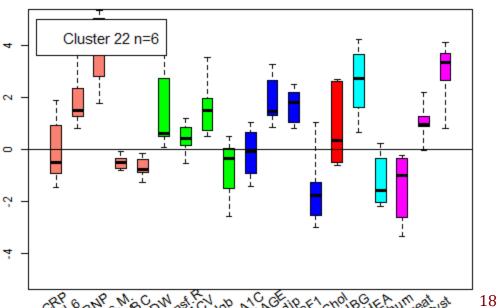
Profile 21:

Cluster:

0% born < 1935;

100% born ≥ 1935; median age 62

67% females



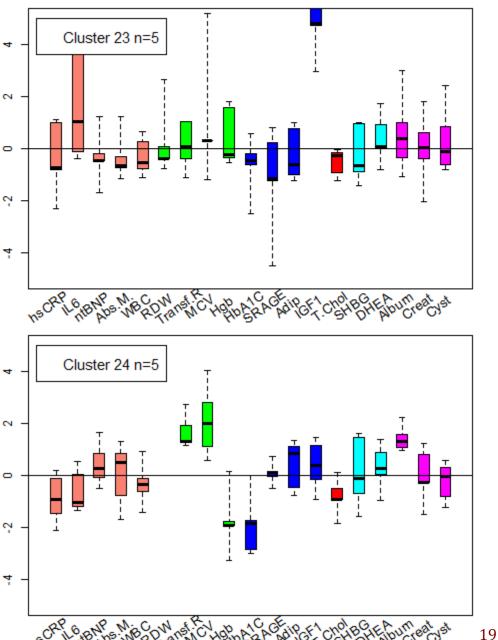
Profile 22:

Cluster:

0% born < 1935;

10% born ≥ 1935; median age 62

50% females



Supplement Figure S16: Profiles 23 and 24

Profile 23:

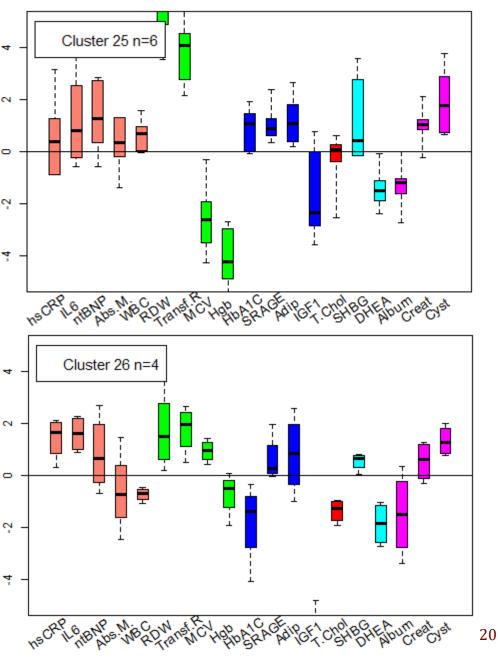
Cluster:

60% born < 1935; median age 90 40% born > 1935; median age 62 80% females

Profile 24:

Cluster:

80% born < 1935; median age 92 20% born ≥ 1935; median age 60 80% females



Supplement Figure S17: Profiles 25 and 26

Profile 25:

Cluster:

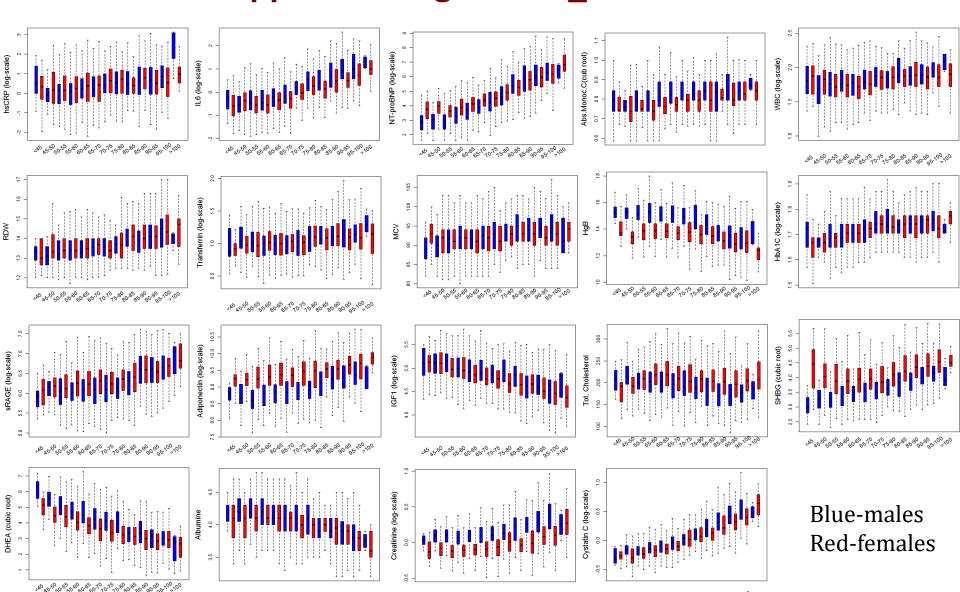
16% born < 1935; median age 84 84% born <u>></u> 1935; median age 64 50% females

Profile 26:

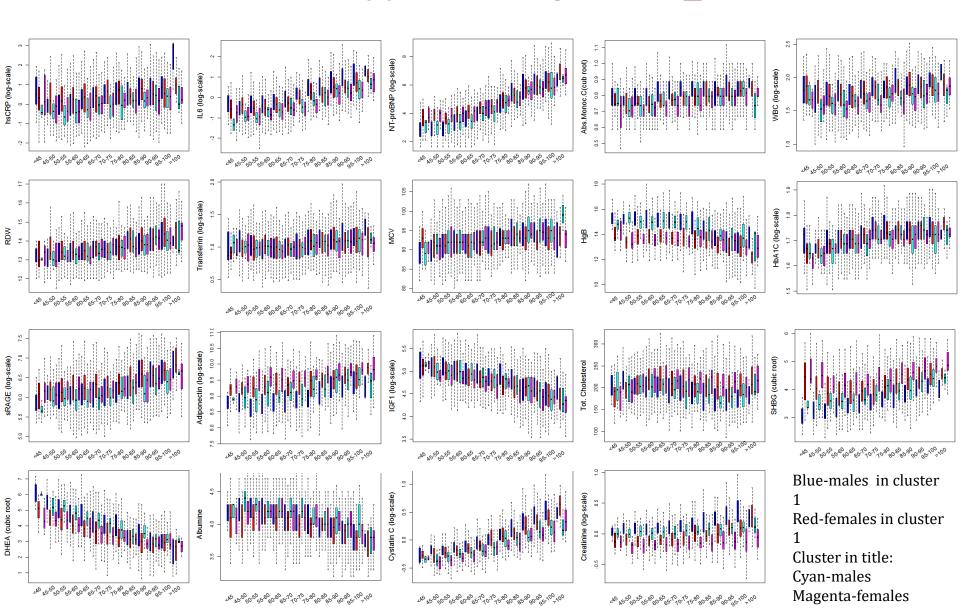
Cluster:

50% born < 1935; median age 97 50% born > 1935; median age 57 50% females

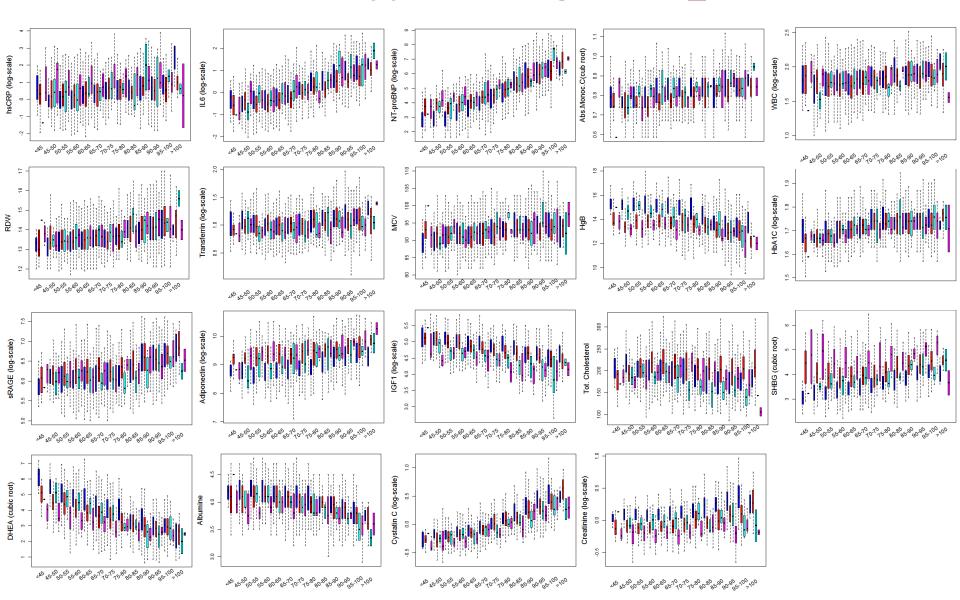
Supplement Figure S18_a: Referent Cluster



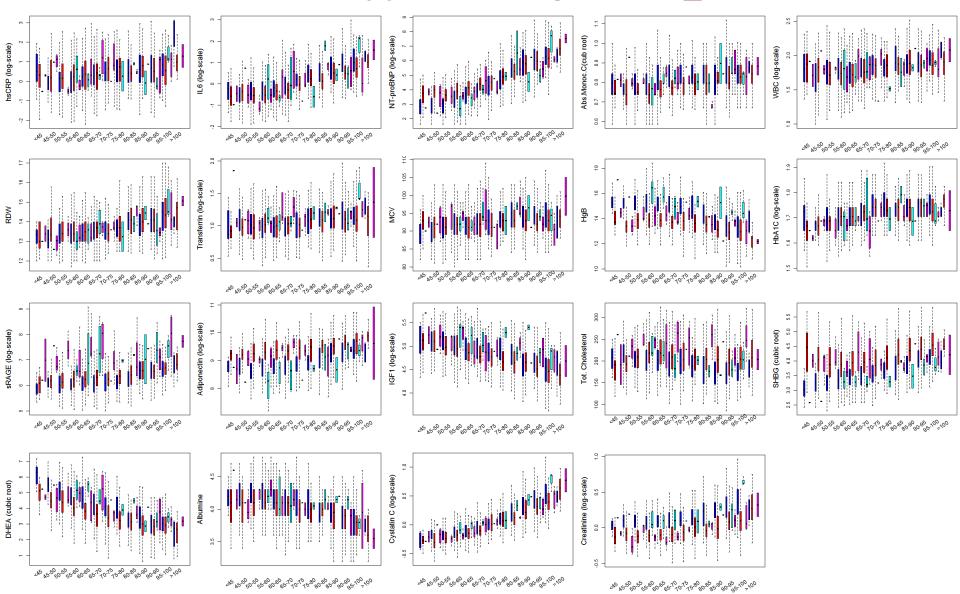
Supplement Figure S18_b: Cluster 2



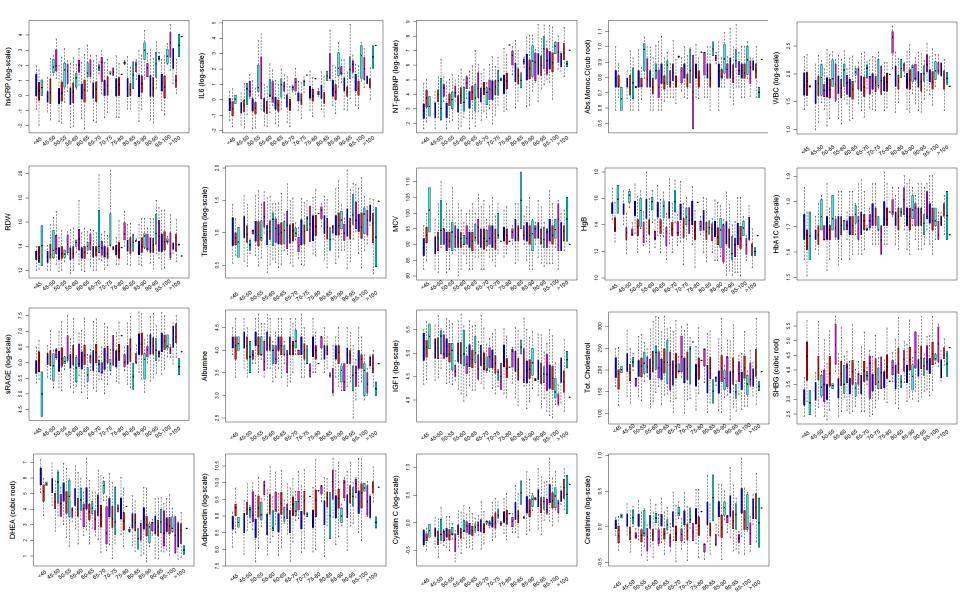
Supplement Figure S18_c: Cluster 3



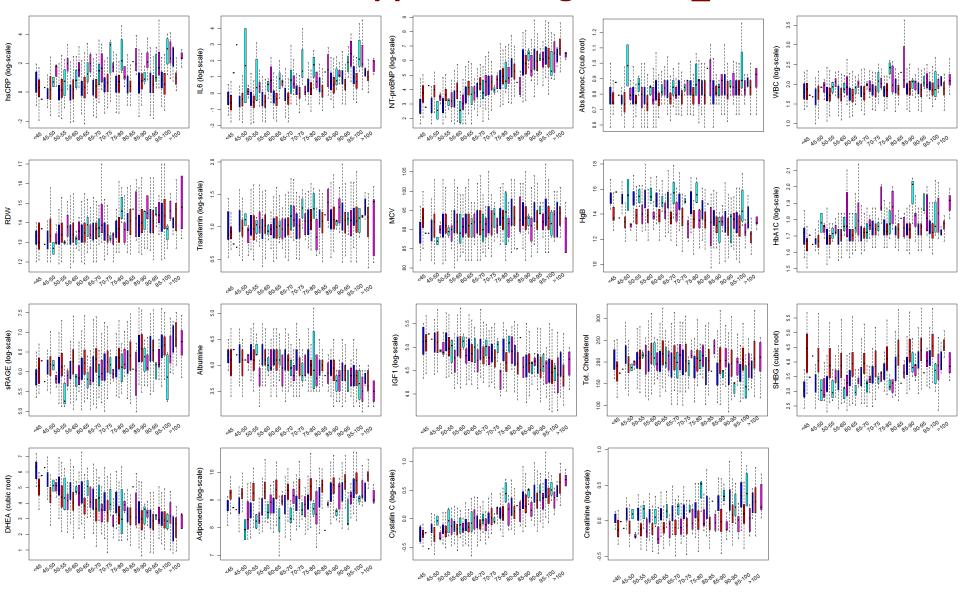
Supplement Figure S18_d: Cluster 4



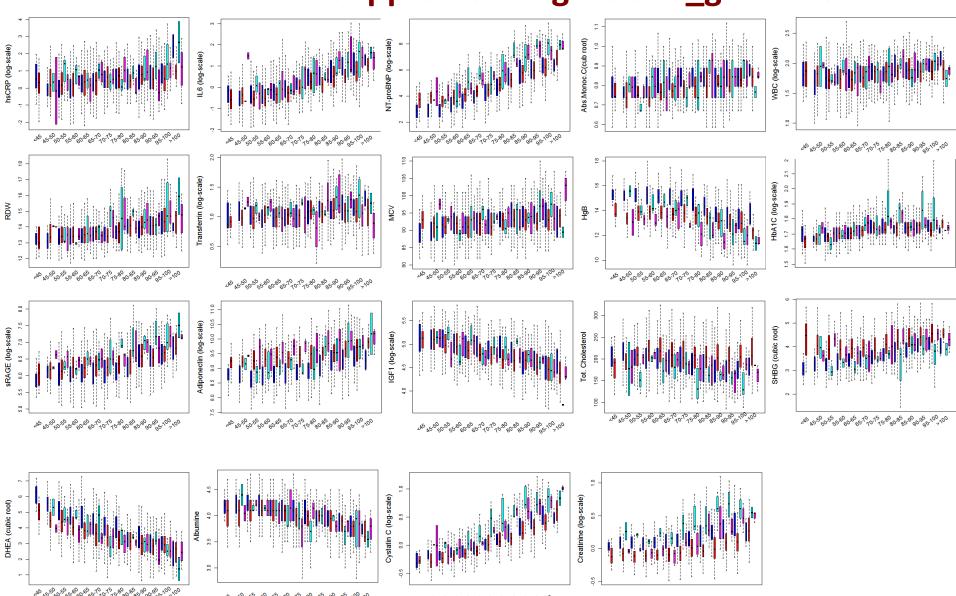
Supplement Figure S18_e: Cluster 5



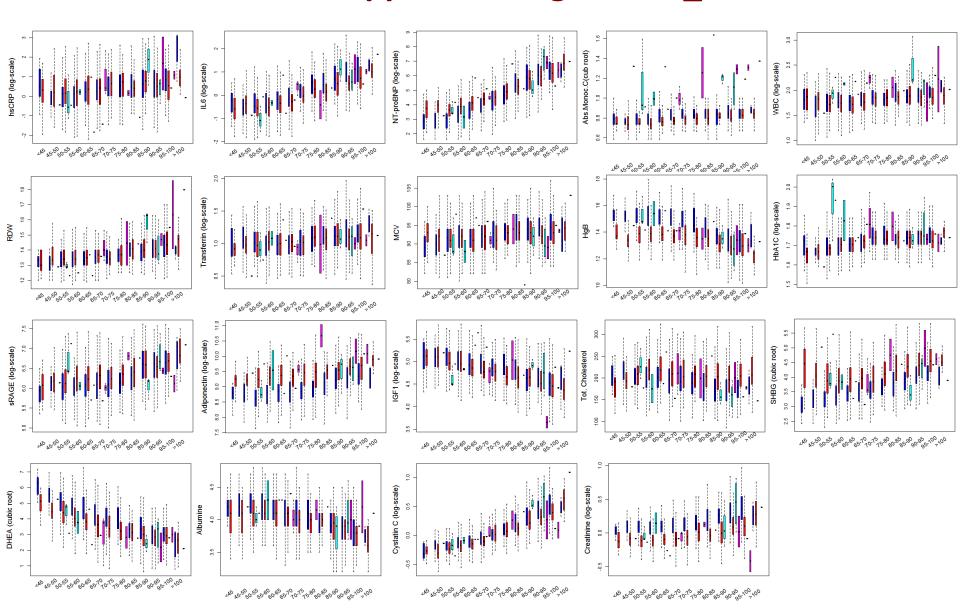
Supplement Figure S18_f: Cluster 6



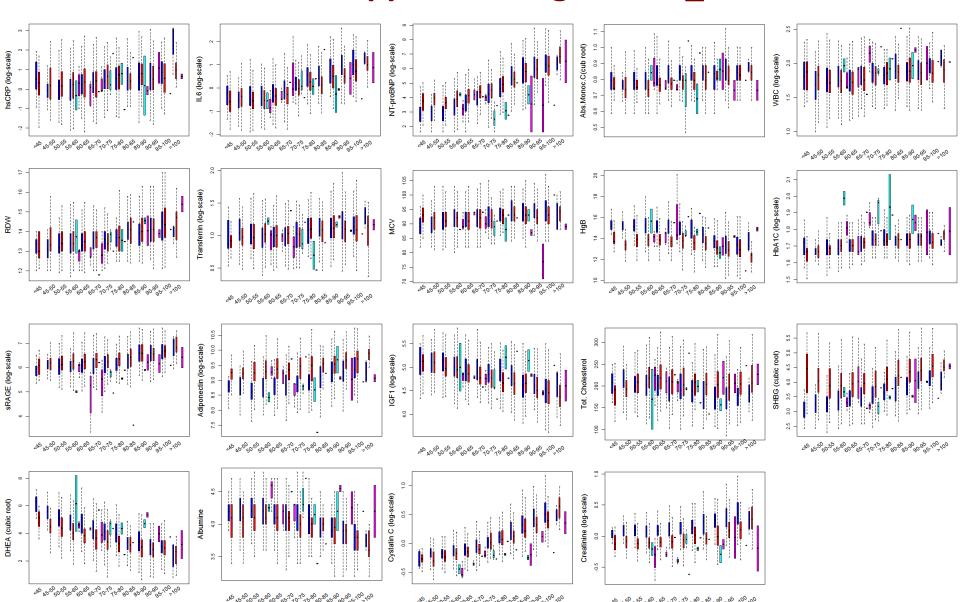
Supplement Figure S18_g: Cluster 7



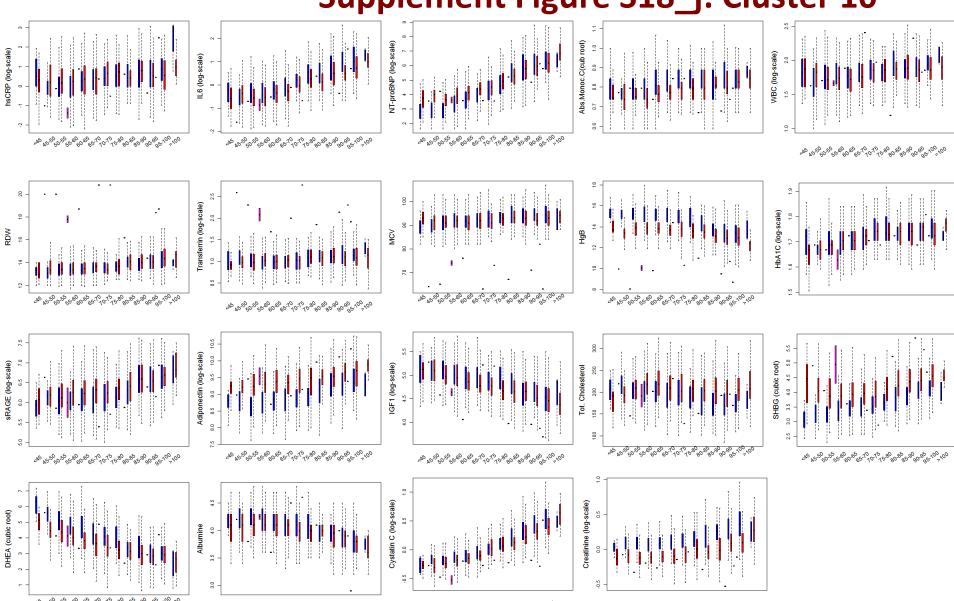
Supplement Figure S18_h: Cluster 8



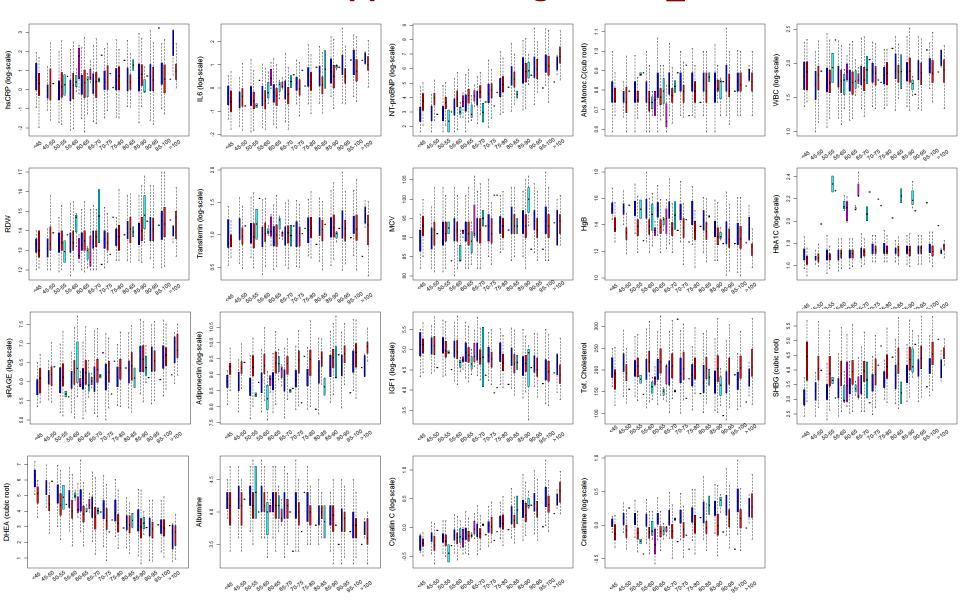
Supplement Figure S18_k: Cluster 9



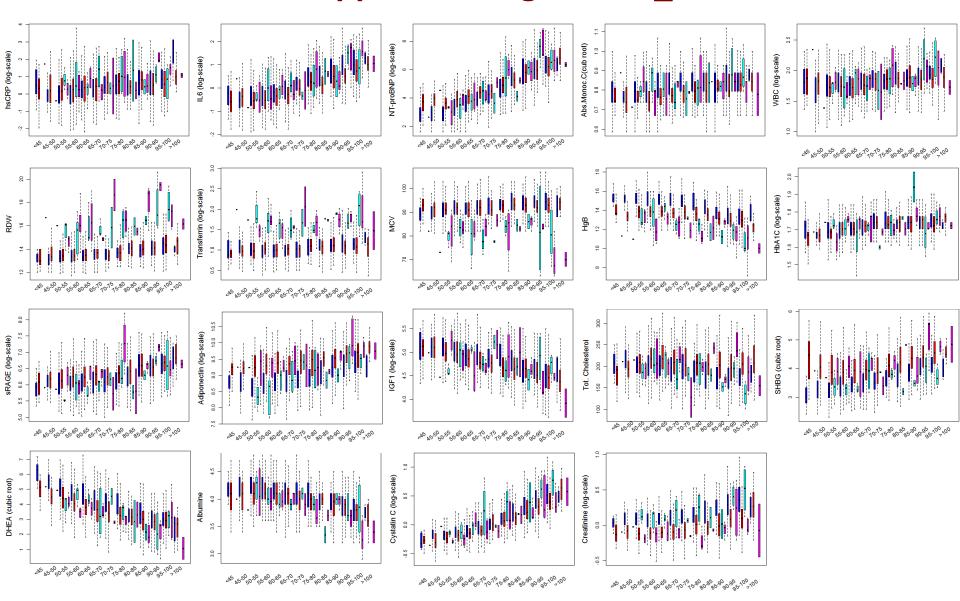
Supplement Figure S18_j: Cluster 10



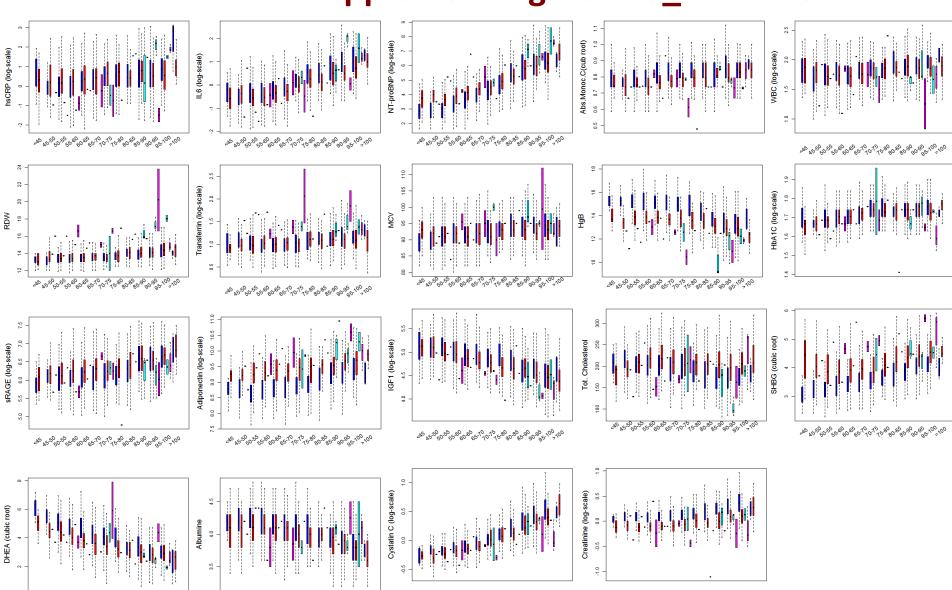
Supplement Figure S18_k: Cluster 11



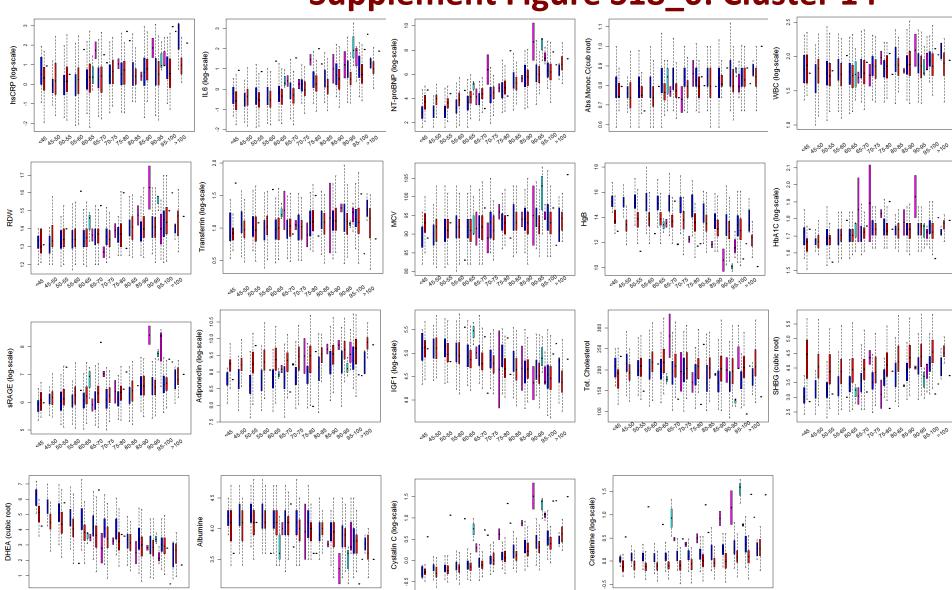
Supplement Figure S18_m: Cluster 12



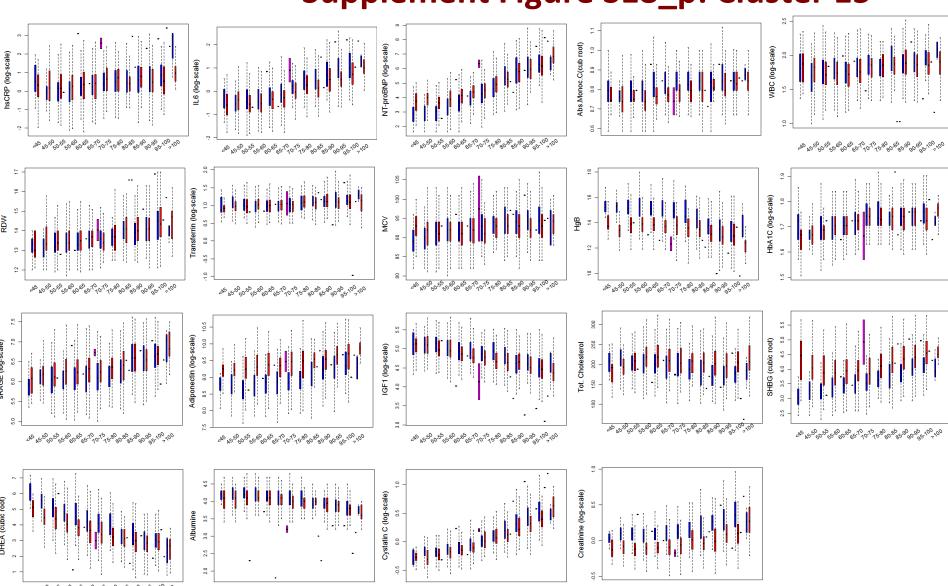
Supplement Figure S18_n: Cluster 13



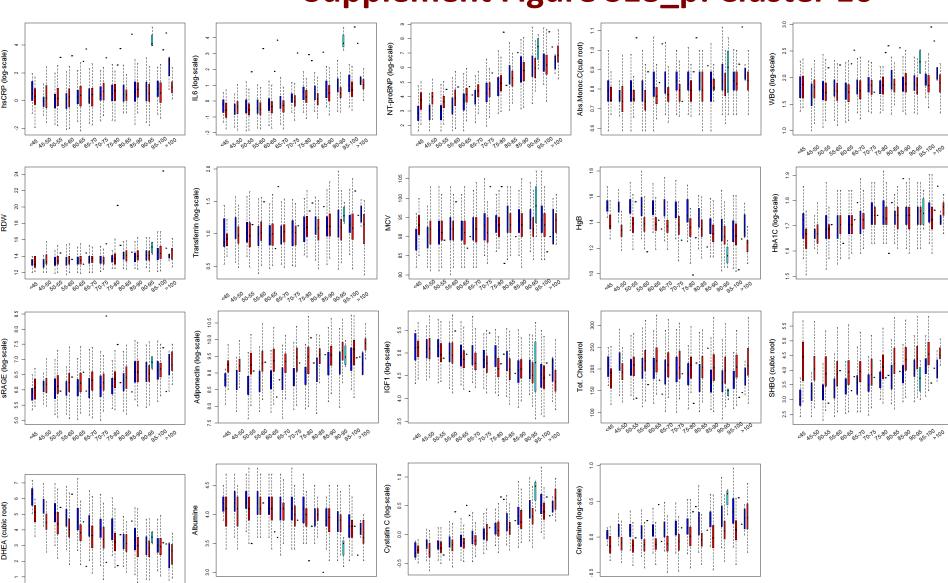
Supplement Figure S18_0: Cluster 14

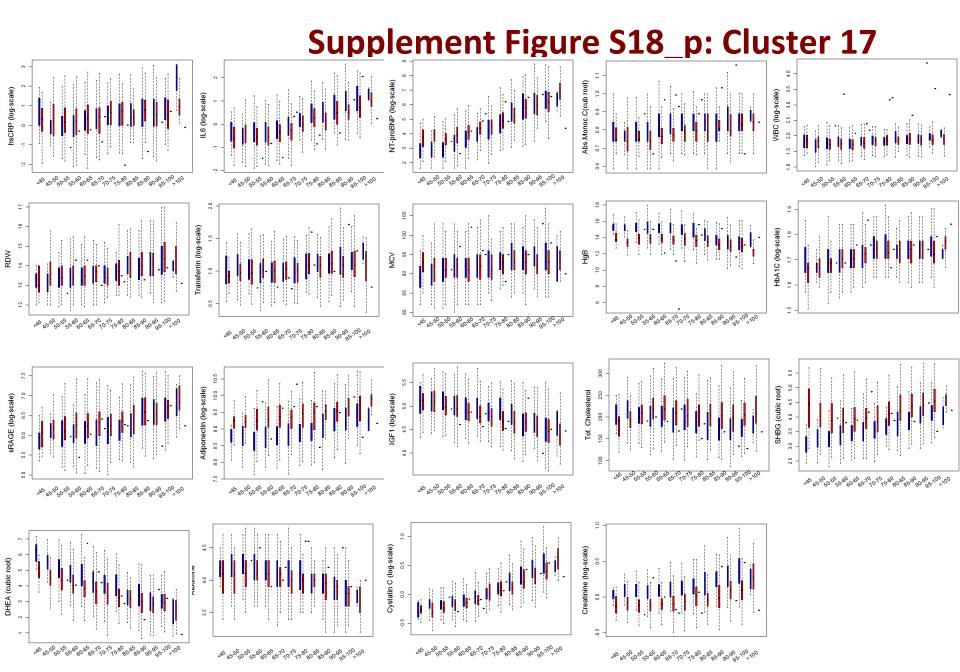


Supplement Figure S18_p: Cluster 15



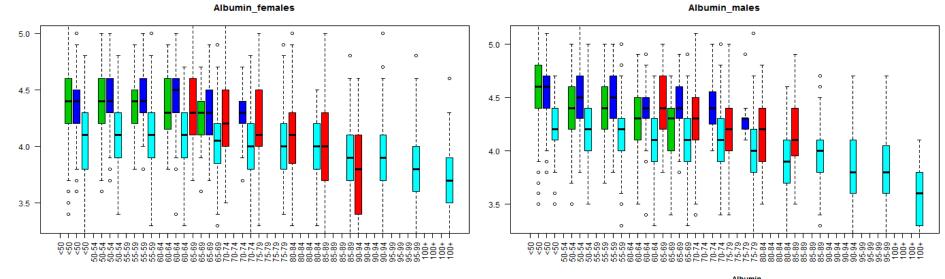
Supplement Figure S18_p: Cluster 16



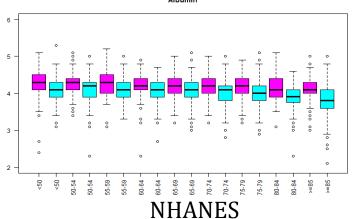


Red=FHS-gen-1 ex20; Green = FHS-gen 2 exam 7; Blue= FHS-gen3 - ex1; Pale blue = LLFS; Normal range 3.5; 5.4

Supplement Figure S19: Example of Lab-to-Lab Bias in Albumin Measurements

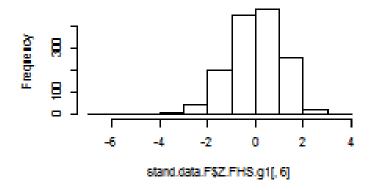


Measurements in FHS tend to be systematically higher at younger ages (batch effect), and converge at older ages. So in older LLFS participants, we see higher than expected albumin. The batch effect is consistent with what we see in NHANES

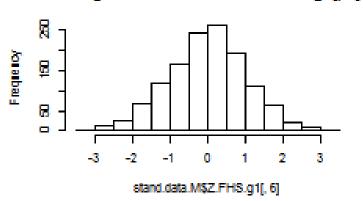


Supplement Figure S20-a: Externally Standardized Adiponectin

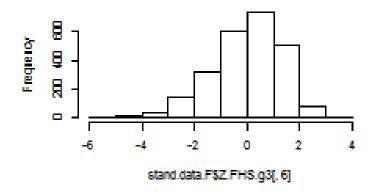
Females
Histogram of stand.data.F\$Z.FHS.g1[, 6]



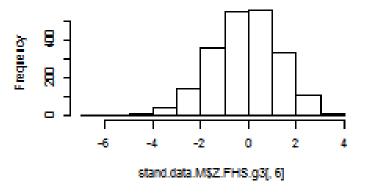
Males
Histogram of stand.data.M\$Z.FHS.g1[, 6]



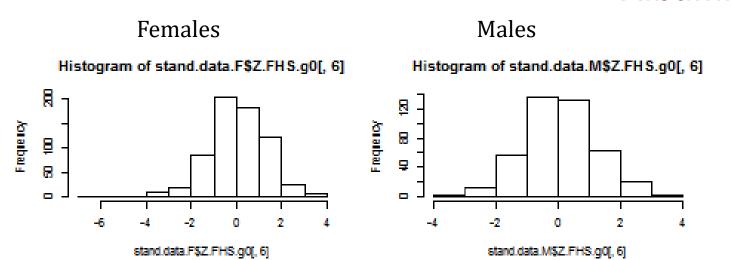
Histogram of stand.data.F\$Z.FHS.g3[, 6]



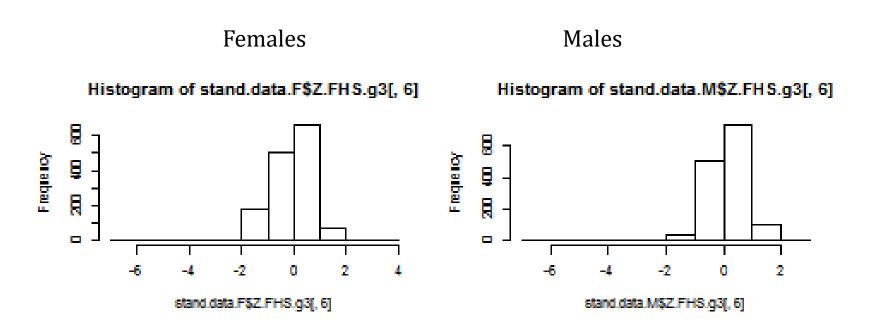
Histogram of stand.data.M\$Z.FHS.q3[, 6]



Supplement Figure S20-b: Externally Standardized Albumin

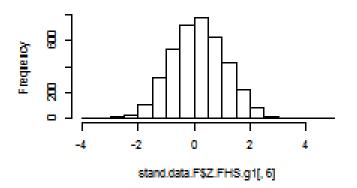


Supplement Figure S20-c: Externally Standardized Abs. Monocyte Counts

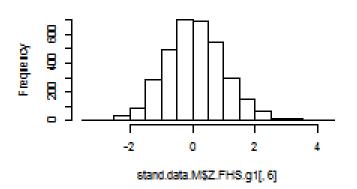


Supplement Figure S20-d: Externally Standardized NT-proBNP

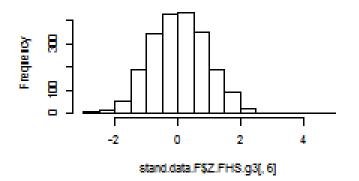
Females
Histogram of stand.data.F\$Z.FHS.g1[, 6]



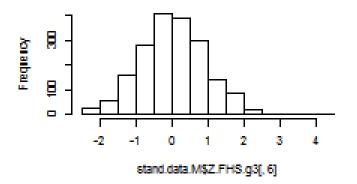
Males
Histogram of stand.data.M\$Z.FHS.q1[, 6]



Histogram of stand.data.F\$Z.FHS.g3[, 6]



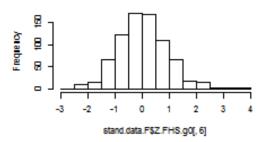
Histogram of stand.data.M\$Z.FHS.q3[, 6]



Supplement Figure S20-e: Externally Standardized Total Cholesterol

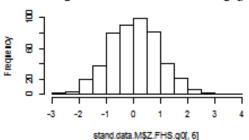
Females

Histogram of stand.data.F\$Z.FHS.g0[, 6]

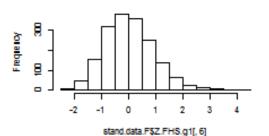


Males

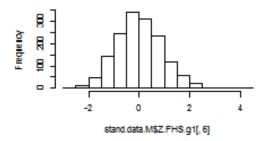
Histogram of stand.data.M\$Z.FHS.g0[, 6]



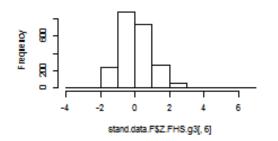
Histogram of stand.data.F\$Z.FHS.g1[, 6]



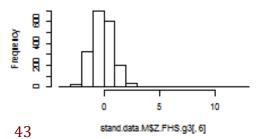
Histogram of stand.data.M\$Z.FHS.g1[, 6]



Histogram of stand.data.F\$Z.FHS.g3[, 6]



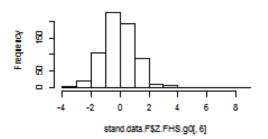
Histogram of stand.data.M\$Z.FHS.g3[, 6]



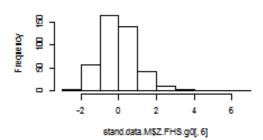
Supplement Figure S20-f: Externally Standardized Creatinine

Females Males

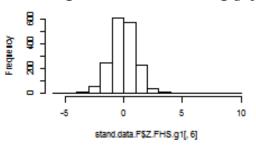




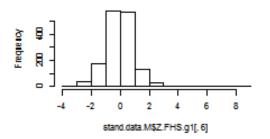
Histogram of stand.data.M\$Z.FHS.g0[, 6]



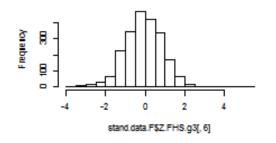
Histogram of stand.data.F\$Z.FHS.g1[, 6]



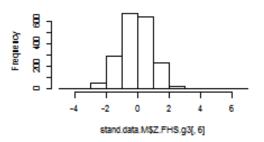
Histogram of stand.data.M\$Z.FHS.g1[, 6]



Histogram of stand.data.F\$Z.FHS.g3[, 6]

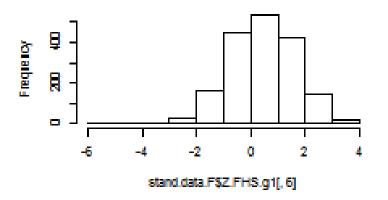


Histogram of stand.data.M\$Z.FHS.g3[, 6]

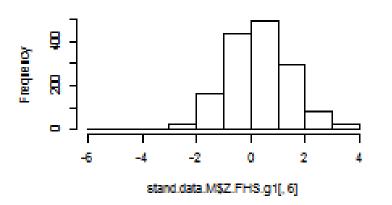


Supplement Figure S20-g: Externally Standardized CRP

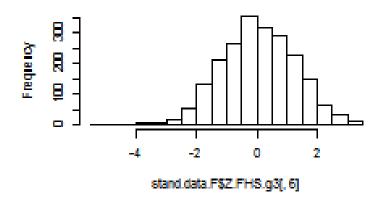
Females
Histogram of stand.data.F\$Z.FHS.g1[, 6]



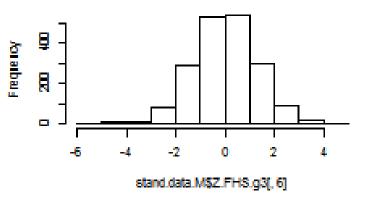
Males
Histogram of stand.data.M\$Z.FHS.q1[, 6]



Histogram of stand.data.F\$Z.FHS.g3[, 6]



Histogram of stand.data.M\$Z.FHS.q3[, 6]



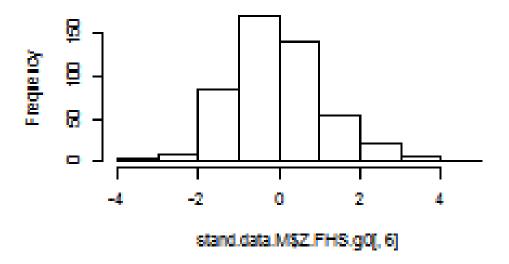
Supplement Figure S20-j: Externally Standardized Cystatin

Females Males Histogram of stand.data.F\$Z.FHS.g1[, 6] Histogram of stand.data.M\$Z.FHS.g1[, 6] B Frequency B Frequency Ħ Ħ o -25 -15 -10 -5 5 -25 -20 -15 -10 -5 5 0 0 stand.data.M\$Z.FHS.q1[, 6] stand.data.F\$Z.FHS.q1[, 6] Histogram of stand.data.F\$Z.FHS.q3[, 6] Histogram of stand.data.M\$Z.FHS.q3[, 6] B 8 Frequency Finding B ₽ -30 -20 -10 0 10 -30 -20 -10 0 stand.data.F\$Z.FHS.g3[, 6] stand.data.M\$Z.FHS.q3[, 6]

Supplement Figure S20-k: Externally Standardized DHEA

Males

Histogram of stand.data.M\$Z.FHS.g0[, 6]



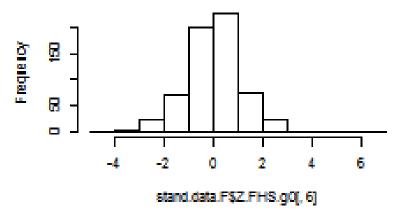
Supplement Figure S20-h: Externally Standardized HbA1C

Females Males Histogram of stand.data.F\$Z.FHS.g0[, 6] Histogram of stand.data.M\$Z.FHS.g0[, 6] R Ħ Frequency Frequency 团 ₽ 8 10 -5 -5 0 5 0 5 10 stand.data.F\$Z.FHS.q0[, 6] stand.data.M\$Z.FHS.q0[, 6] Histogram of stand.data.F\$Z.FHS.q1[, 6] Histogram of stand.data.M\$Z.FHS.q1[, 6] 8 Frequency Frequency ₽ ₽ -15 -10 -5 5 15 10 0 10 stand.data.F\$Z.FHS.g1[, 6] stand.data.M\$Z.FHS.q1[, 6]

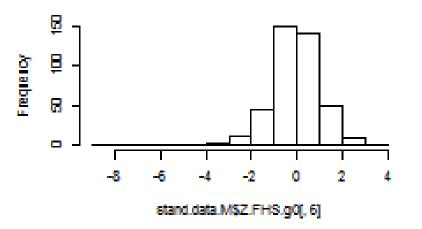
Supplement Figure S20-m: Externally Standardized HGB

Females Males

Histogram of stand.data.F\$Z.FHS.g0[, 6]

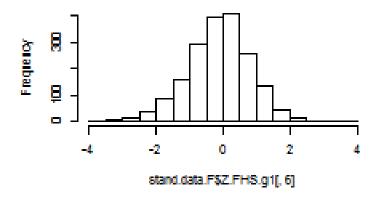


Histogram of stand.data.M\$Z.FHS.g0[, 6]

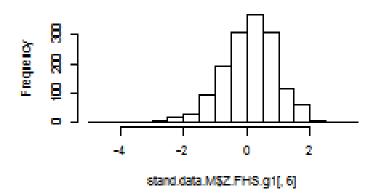


Supplement Figure S20-n: Externally Standardized IGF1

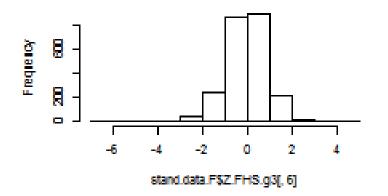
Females
Histogram of stand.data.F\$Z.FHS.g1[, 6]



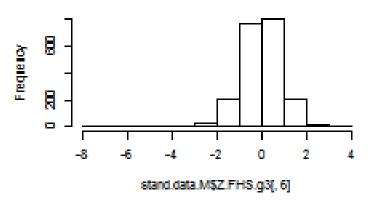
Males
Histogram of stand.data.M\$Z.FHS.g1[, 6]



Histogram of stand.data.F\$Z.FHS.g3[, 6]

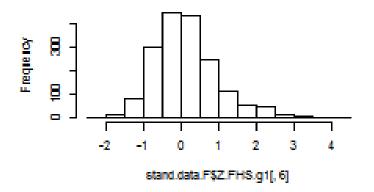


Histogram of stand.data.M\$Z.FHS.g3[, 6]

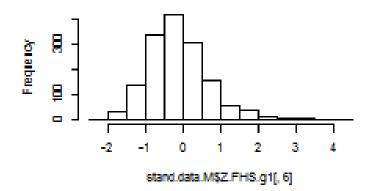


Supplement Figure S20-p: Externally Standardized IL6

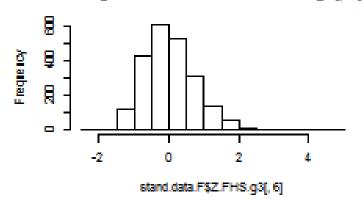
Females
Histogram of stand.data.F\$Z.FHS.g1[, 6]



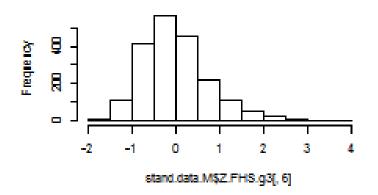
Males
Histogram of stand.data.M\$Z.FHS.g1[, 6]



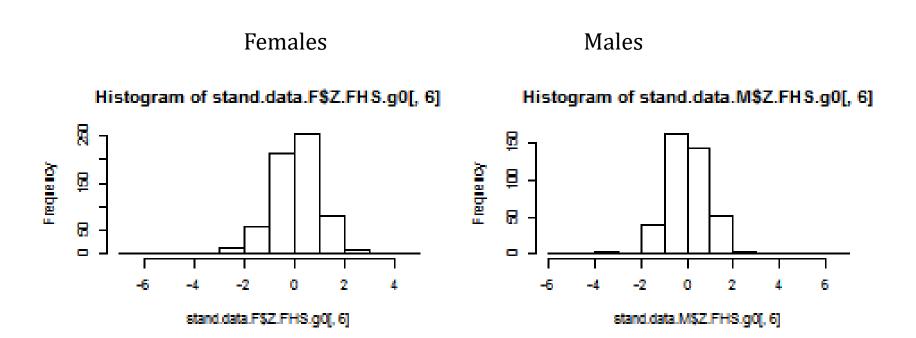
Histogram of stand.data.F\$Z.FHS.g3[, 6]



Histogram of stand.data.M\$Z.FHS.g3[, 6]

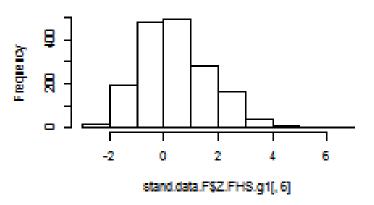


Supplement Figure S20-q: Externally Standardized MCV

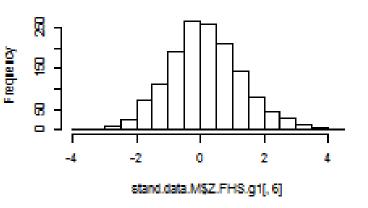


Supplement Figure S20-r: Externally Standardized SHBG

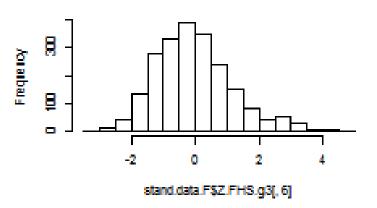
Females
Histogram of stand.data.F\$Z.FHS.g1[, 6]



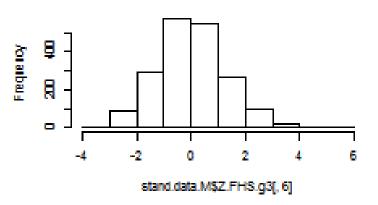
Males
Histogram of stand.data.M\$Z.FHS.g1[, 6]



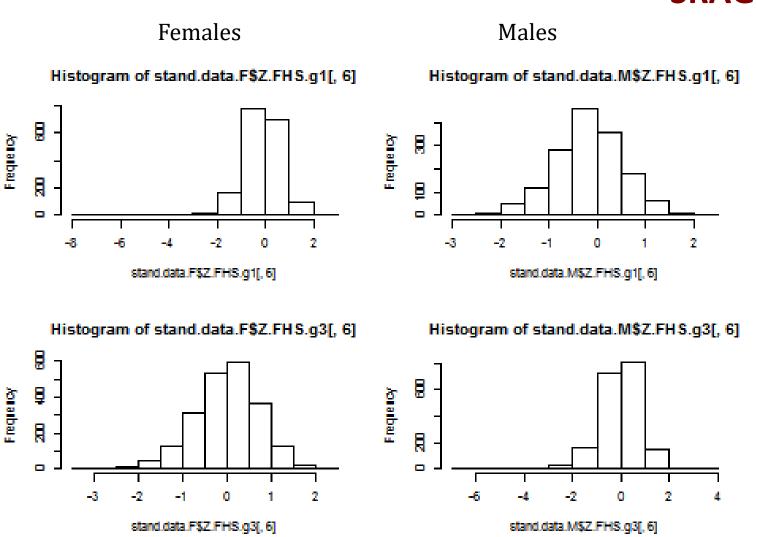
Histogram of stand.data.F\$Z.FHS.g3[, 6]



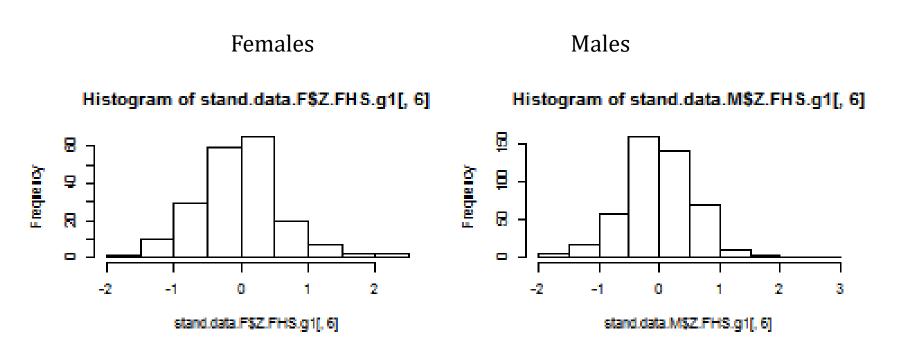
Histogram of stand.data.M\$Z.FHS.g3[, 6]



Supplement Figure S20-s: Externally Standardized SRAGE

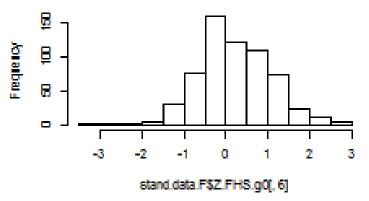


Supplement Figure S20-v: Externally Standardized Transferrin

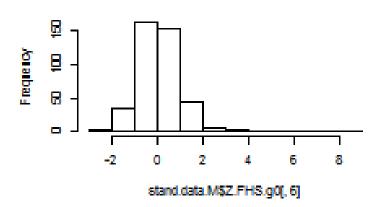


Supplement Figure S20-w: Externally Standardized WBC

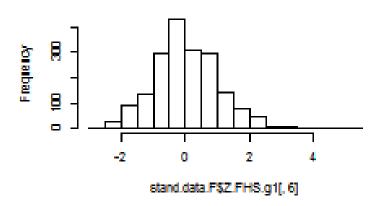
Females
Histogram of stand.data.F\$Z.FHS.g0[, 6]



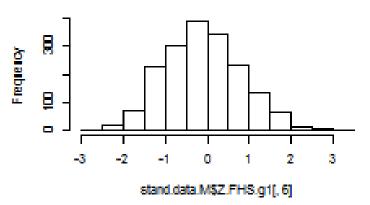
Males
Histogram of stand.data.M\$Z.FHS.g0[, 6]



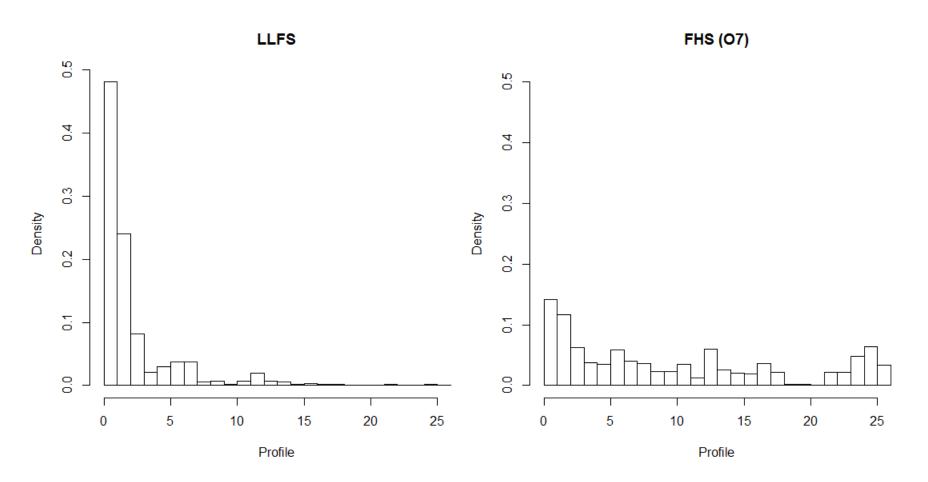
Histogram of stand.data.F\$Z.FHS.g1[, 6]



Histogram of stand.data.M\$Z.FHS.q1[, 6]



Supplement Figure S21: Distribution of Biomarker Signatures in LLFS and FHS



We see many more "anomalous patterns" in FHS

Figure S22-a Biomarker Signatures 1-4 in FHS

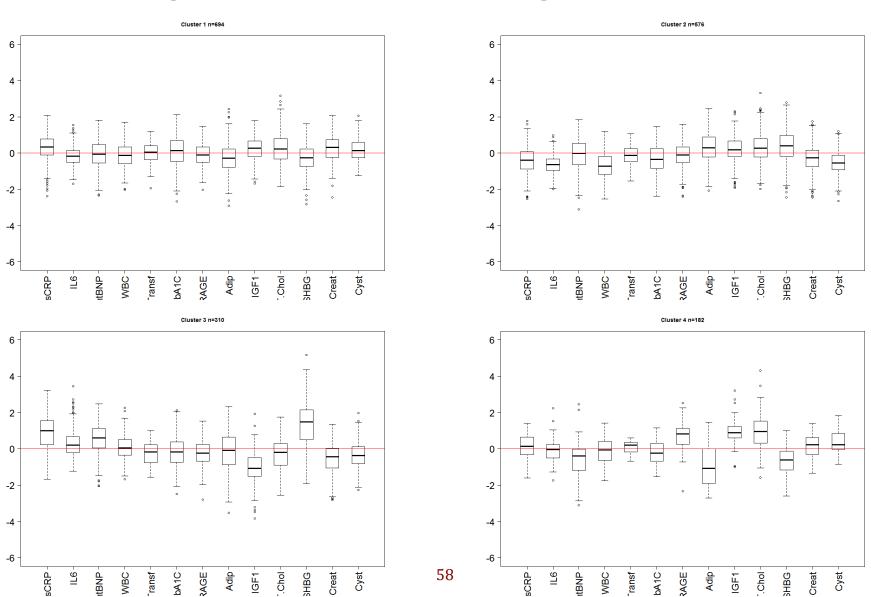


Figure S22-b Biomarker Signatures 5-8 in FHS

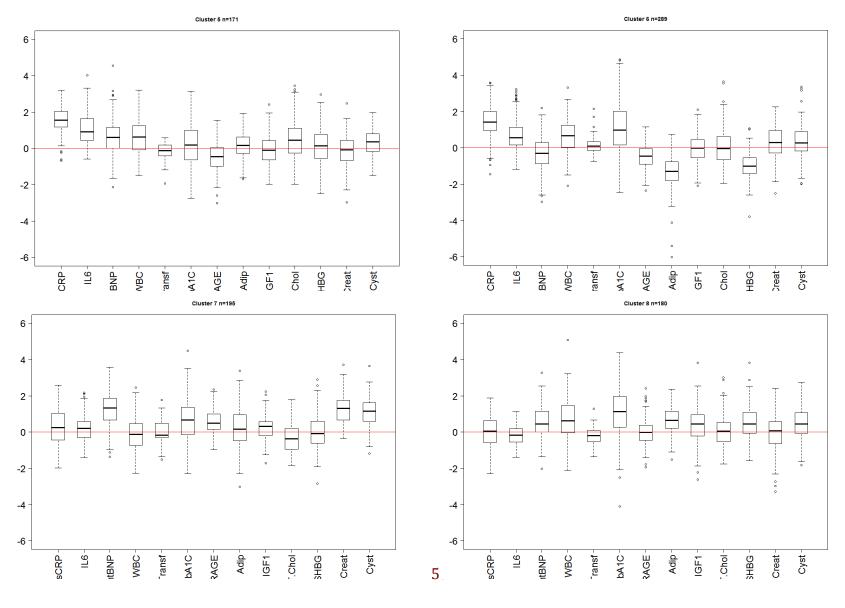


Figure S22-c Biomarker Signatures 9-12 in FHS

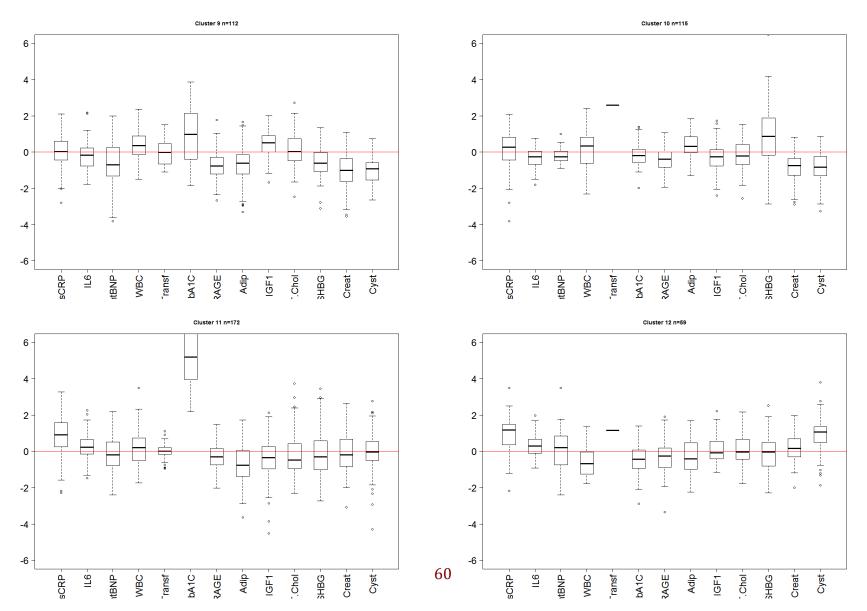


Figure S22-d Biomarker Signatures 13-16 in FHS

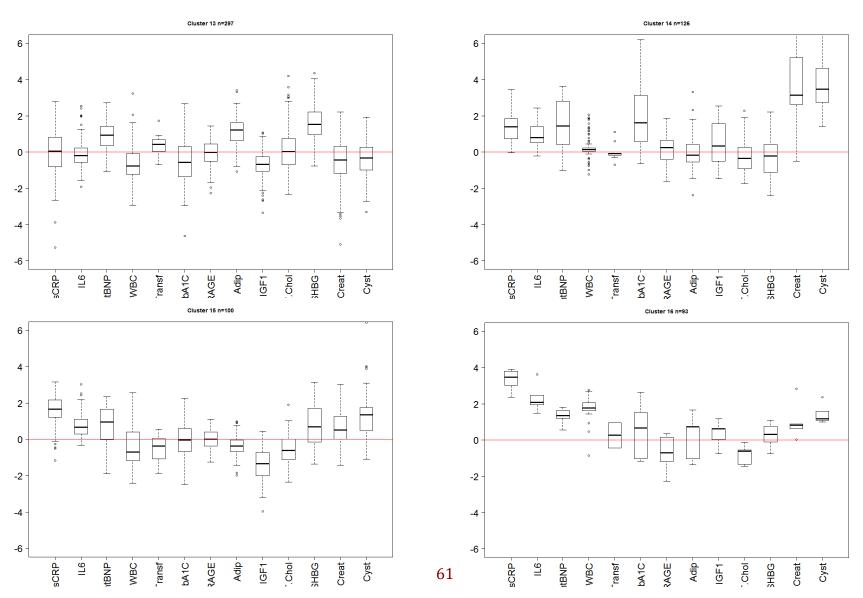


Figure S22-e Biomarker Signatures 17-20 in FHS

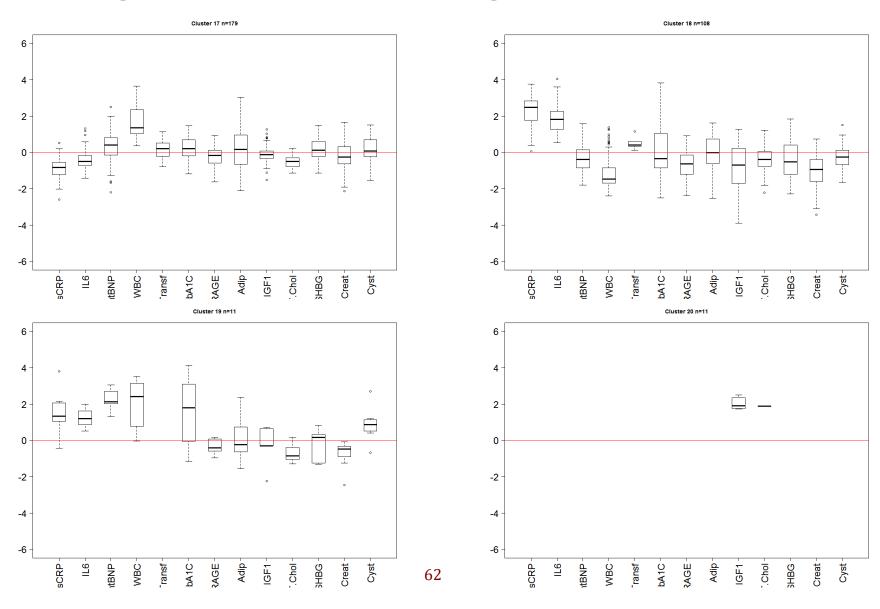


Figure S22-f Biomarker Signatures 21-24 in FHS

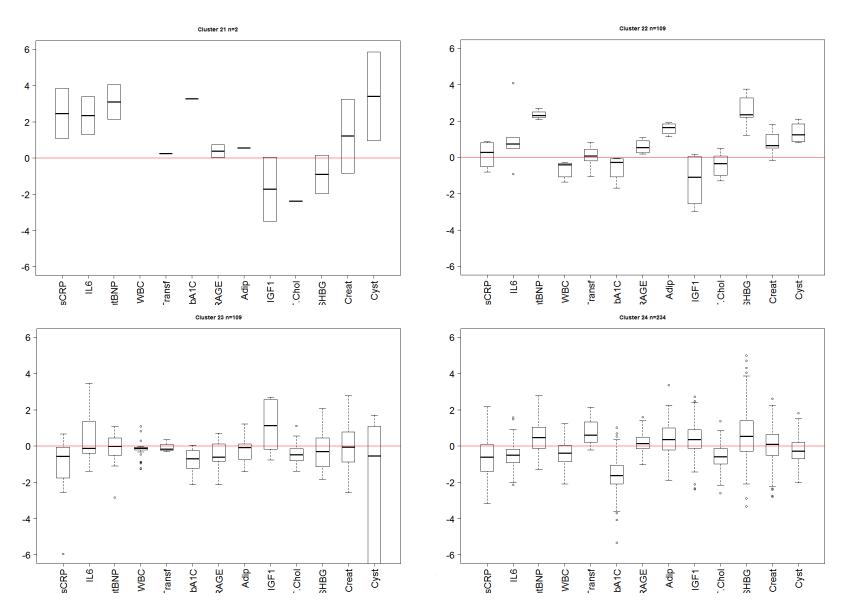


Figure S22-g Biomarker Signatures 25, 26 in FHS

